

IN THE CLAIMS

This listing of claims will replace all prior versions and listings of claims in the present application:

1-59. (Cancelled)

60. (Currently Amended) A method for ~~synthesizing~~ preparing one or more cDNA molecules from one or more RNA templates, the method comprising incubating said RNA templates in a buffer solution containing dNTPs, ~~and one or more primers complementary to at least a portion of one or more of the RNA templates, at least 1 mM magnesium ions, in the substantial absence of manganese ions, and with a purified polypeptide DNA polymerase that exhibits the an amino acid sequence exhibited by the a full-length DNA polymerase derived from a *Bacillus stearothermophilus* (Bst) type strain 5 in the presence of at least 1 mM magnesium ions and in the substantial absence of manganese ions, whereby selected from the group consisting of ATCC strain # 12016 and ATCC strain # 12980, under conditions wherein cDNA molecules complementary to one or more of the RNA templates are synthesized~~ obtained ~~and wherein the purified DNA polymerase is full-length Bst type strain 5 DNA polymerase.~~

61. (Currently Amended) A method for ~~synthesizing~~ preparing one or more cDNA molecules from one or more RNA templates, the method comprising incubating said RNA templates in a buffer solution containing dNTPs, ~~and one or more primers complementary to at least a portion of one or more of the RNA templates, at least 1 mM magnesium ions, in the substantial absence of manganese ions, and with a purified DNA polymerase in the presence of at least 1 mM magnesium ions and in the substantial absence of manganese ions, whereby cDNA molecules complementary to one or more of the RNA templates are obtained, wherein the a purified polypeptide that DNA polymerase exhibits the an amino acid sequence exhibited by is the a subtilisin digestion product of a full-length DNA polymerase derived from a *Bacillus*~~

stearothermophilus (Bst)-type strain selected from the group consisting of ATCC strain # 12016 and ATCC strain # 12980, 5-DNA polymerase, wherein said subtilisin digestion product that: (a) has a mass of about 55 to about 65 kDA as determined by 10% SDS PAGE;₃ (b) lacks 5'-to-3' exonuclease activity;₃ and (c) has reverse transcriptase activity in the presence of magnesium ions and in the substantial absence of manganese ions, under conditions wherein cDNA molecules complementary to one or more of the RNA templates are synthesized.

62. (Cancelled)

63. (Previously Presented) The method of claim 61 wherein the magnesium ion concentration is about 1 mM to about 10 mM.

64. (Previously Presented) The method of claim 61 wherein the primers that are complementary to at least a portion of the RNA templates are selected from the group consisting of: (a) target-specific primers; (b) oligo(dT) primers; and (c) random primers.

65. (Cancelled)

66. (Previously Presented) The method of claim 60 wherein the magnesium ion concentration is about 1 mM to about 10 mM.

67. (Previously Presented) The method of claim 60 wherein the primers that are complementary to at least a portion of the RNA templates are selected from the group consisting of: (a) target-specific primers; (b) oligo(dT) primers; and (c) random primers.

68-70. (Cancelled)

U.S. Pat. Appn. No. 09/979,518
Art Unit 1652
Response and RCE to Sept. 28, 2009 Final Office Action

71. (New) The method of claim 60, further comprising using one or more of the one or more cDNA molecules that are synthesized as templates for amplifying one or more of the one or more RNA templates using PCR or a transcription-based amplification technique.

72. (New) The method of claim 71 wherein the transcription-based amplification technique is selected from the group consisting of NASBA, TMA, 3SR, and SPSR.

73. (New) The method of claim 61, further comprising using one or more of the one or more cDNA molecules that are synthesized as templates for amplifying one or more of the one or more RNA templates using PCR or a transcription-based amplification technique.

74. (New) The method of claim 73 wherein the transcription-based amplification technique is selected from the group consisting of NASBA, TMA, 3SR, and SPSR.